

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,844
Source: PT/10
Date Processed by STIC: 4/4/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/04/2005

PATENT APPLICATION: US/10/528,844

TIME: 11:02:09

Input Set : A:\0185658SeqList.txt

Output Set: N:\CRF4\04042005\J528844.raw

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3 <110> APPLICANT: F. HOFFMANN-LA ROCHE AG
5 <120> TITLE OF INVENTION: DNA encoding FAD dependent D-erythronic acid
6     4-phosphohate dehydrogenase involved in vitamin B6
7     biosynthesis
9 <130> FILE REFERENCE: sequence for pdxR (case19)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/528,844
C--> 12 <141> CURRENT FILING DATE: 2005-03-23
14 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1491
20 <212> TYPE: DNA
21 <213> ORGANISM: Sinorhizobium meliloti
23 <400> SEQUENCE: 1
24 atggccatcg gcacgcttga agcaaccacg ttgatccgag gcagggccat gaccaccgta 60
25 cttccttctc ccgaactcat cgctccttc gtcgatatcg tcgggcctgg caatgccctc 120
26 accgcacccg ccgacacggc accctacctc gtcgagtcgc gcgggctcta ccgcggcacg 180
27 acgccgctcg tgctcaggcc cggctccgtc gaggaagttt cgctggtgat gcggcttgcg 240
28 agtcagaccc gaacggcagt cgtgccgcag ggcggcaata ccggacatgt ggccggacag 300
29 attccacgcy agggcaaagc cgacgtggtc ctttcctctg agcggctgaa ccgcatccgc 360
30 gacatcgacc cggtcggcaa cgtgatcggt gccgacgcgc gctgtatcct ggccggacatc 420
31 cagaaggccg ccgatgacgt cgaccggctt tttccctgt cactcggctc ggaaggctct 480
32 gcccggatcg gcggcaatct ttcgaccaat gccggcggca ctgccgtgct tgcctatggg 540
33 aacatgcgcc agctctgcct ggggctggaa gtcgtgctcc cgaccgggga gatctgggat 600
34 gggctcagac gcctcaggaa ggacaatacc ggctacgatc tgccgcatct tttcatcggc 660
35 gccgagggaa cgctcggcgt cataaccggc gccgttttga agctctttcc gaaaccgcgc 720
36 ggccaccagg tggcctttgc cggcctcagg agcgtcagg acgcacttac gcttttcgat 780
37 cgggcaacaa gcgtctgcgg gccggccctg acgggcttcg aactgatgcc gcggctcggc 840
38 atcgagttca ccaccggca catcgccggc gtcagagatc cgatggaaac gacgcatccg 900
39 tggtagcgcg tgatcgatat ctccacctcg gataccgcgc aaagcgcgga acggatggtg 960
40 caagaccttc tcgaagccgt cattgccgac ggtctcgtcg aaaacgcggt catcgcccag 1020
41 aacgaagcgc aacgcagagc gctctggcac atgcgagaaa gcatgtcgcc ggcacaaaag 1080
42 cctgaggggtg gctccatcaa gcatgacggt tcggtcccgg tgctcagcat tccggccttc 1140
43 atgacggagg cggatgcgct ggtctccaag gccatccccg gcgcgcgcat ctgcgccttc 1200
44 ggccatatgg gcgacggcaa tatccactac aacatctccc agcccgtcgg cgcggacaag 1260
45 cagagctttc tcgatcgggtg gcgcgagatc aatgcgacgt ttcacgccgt cgtgctcaaa 1320
46 catgacggct cgatctctgc cgagcatggc atcgccaggt tgaagcgaga cgaactcgcg 1380
47 gcgatccgct cgccgatcga gatcgagctc atgcgacgga tcaagcacgc cttcgaccgc 1440
48 gcggggatca tgaaccccga taaggtgctg cgcgaggatc gaggcgagta a 1491
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 496
53 <212> TYPE: PRT
54 <213> ORGANISM: Sinorhizobium meliloti

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56 <400> SEQUENCE: 2

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57 Met Ala Ile Gly Thr Leu Glu Ala Thr Thr Leu Ile Arg Gly Arg Ala
58                               5                               10                               15
59 Met Thr Thr Val Leu Pro Ser Pro Glu Leu Ile Ala Ser Phe Val Asp
60                               20                               25                               30
61 Ile Val Gly Pro Gly Asn Ala Leu Thr Ala Pro Ala Asp Thr Ala Pro
62                               35                               40                               45
63 Tyr Leu Val Glu Ser Arg Gly Leu Tyr Arg Gly Thr Thr Pro Leu Val
64                               50                               55                               60
65 Leu Arg Pro Gly Ser Val Glu Glu Val Ser Leu Val Met Arg Leu Ala
66 65                               70                               75                               80
67 Ser Gln Thr Arg Thr Ala Val Val Pro Gln Gly Gly Asn Thr Gly His
68                               85                               90                               95
69 Val Ala Gly Gln Ile Pro Arg Glu Gly Lys Ala Asp Val Val Leu Ser
70                               100                              105                              110
71 Leu Glu Arg Leu Asn Arg Ile Arg Asp Ile Asp Pro Val Gly Asn Val
72                               115                              120                              125
73 Ile Val Ala Asp Ala Gly Cys Ile Leu Ala Asp Ile Gln Lys Ala Ala
74                               130                              135                              140
75 Asp Asp Val Asp Arg Leu Phe Pro Leu Ser Leu Gly Ser Glu Gly Ser
76 145                              150                              155                              160
77 Ala Arg Ile Gly Gly Asn Leu Ser Thr Asn Ala Gly Gly Thr Ala Val
78                               165                              170                              175
79 Leu Ala Tyr Gly Asn Met Arg Gln Leu Cys Leu Gly Leu Glu Val Val
80                               180                              185                              190
81 Leu Pro Thr Gly Glu Ile Trp Asp Gly Leu Arg Arg Leu Arg Lys Asp
82                               195                              200                              205
83 Asn Thr Gly Tyr Asp Leu Arg Asp Leu Phe Ile Gly Ala Glu Gly Thr
84                               210                              215                              220
85 Leu Gly Val Ile Thr Gly Ala Val Leu Lys Leu Phe Pro Lys Pro Arg
86 225                              230                              235                              240
87 Gly His Gln Val Ala Phe Ala Gly Leu Arg Ser Val Glu Asp Ala Leu
88                               245                              250                              255
89 Thr Leu Phe Asp Arg Ala Thr Ser Val Cys Gly Pro Ala Leu Thr Gly
90                               260                              265                              270
91 Phe Glu Leu Met Pro Arg Leu Gly Ile Glu Phe Thr Thr Arg His Ile
92                               275                              280                              285
93 Ala Gly Val Arg Asp Pro Met Glu Thr Thr His Pro Trp Tyr Ala Leu
94                               290                              295                              300
95 Ile Asp Ile Ser Thr Ser Asp Thr Ala Glu Ser Ala Glu Arg Met Val
96 305                              310                              315                              320
97 Gln Asp Leu Leu Glu Ala Val Ile Ala Asp Gly Leu Val Glu Asn Ala
98                               325                              330                              335
99 Val Ile Ala Gln Asn Glu Ala Gln Arg Arg Ala Leu Trp His Met Arg
100                              340                              345                              350
101 Glu Ser Met Ser Pro Ala Gln Lys Pro Glu Gly Gly Ser Ile Lys His
102                              355                              360                              365
103 Asp Val Ser Val Pro Val Ser Ser Ile Pro Ala Phe Met Thr Glu Ala
104                              370                              375                              380

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105 Asp Ala Leu Val Ser Lys Ala Ile Pro Gly Ala Arg Ile Cys Ala Phe
106 385                      390                      395                      400
107 Gly His Met Gly Asp Gly Asn Ile His Tyr Asn Ile Ser Gln Pro Val
108                      405                      410                      415
109 Gly Ala Asp Lys Gln Ser Phe Leu Asp Arg Trp Arg Glu Ile Asn Ala
110                      420                      425                      430
111 Ile Val His Ala Val Val Leu Lys His Asp Gly Ser Ile Ser Ala Glu
112                      435                      440                      445
113 His Gly Ile Gly Gln Leu Lys Arg Asp Glu Leu Ala Ala Ile Arg Ser
114                      450                      455                      460
115 Pro Ile Glu Ile Glu Leu Met Arg Arg Ile Lys His Ala Phe Asp Pro
116 465                      470                      475                      480
117 Ala Gly Ile Met Asn Pro Asp Lys Val Leu Arg Glu Asp Arg Gly Glu
118                      485                      490                      495
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 19
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
128     synthesized primer sequence
130 <400> SEQUENCE: 3
131 gaattcatgg ccatcgga                                19
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 23
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
141     synthesized primer sequence
143 <400> SEQUENCE: 4
144 ccacttcct ttagtacga gct                                23

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date